

**CLAIM AMENDMENT**

Please amend the claims in accordance with the following listing.

**Listing of Claims:**

1. (Currently Amended) A method including
  - ~~executing, on a computing device, an autonomous software element, said autonomous software element having access to accessing information about a plurality of gene expression values; generating, in response to said information, generating from said information a hypothesized relationship about genes associated with said gene expression values, said hypothesized relationship having the properties of being (1) relatively unlikely to be a likelihood of being due to chance not exceeding a predetermined value; chance, and (2) relatively likely to be of interest to retrieving data regarding interests of each agent of a plurality of agents; identifying at least one agent of the plurality of agents such that the data regarding interests of said at least one agent satisfies at least one predetermined test indicating that said at least one agent has a potential interest in the hypothesized relationship; and other than said autonomous software element;~~
  - sending information about said hypothesized relationship to said at least one agent.
  
2. (Currently Amended) A method as in claim 1, including collecting said information about the plurality of gene expression values from a plurality of relatively nonlocal external databases.

3. (Currently Amended) A method as in claim 1, including collecting said information from at least one ~~relatively nonlocal~~ external database.

4. (Original) A method as in claim 1, wherein generating includes selecting a first set of genes in response to said gene expression values; selecting a second set of genes in response to data other than said gene expression values; applying a statistical technique to said first set and said second set; and confirming said hypothesized relationship in response to applying said statistical technique.

5. (Original) A method as in claim 1, wherein generating includes selecting a set of genes in response to said gene expression values; comparing the frequencies of the nucleotide sequences upstream from said set of genes to the frequencies of the nucleotide sequences upstream of genes not in said set; and constructing a hypothesis that is responsive to sequences that have an anomalous frequency distribution.

6. (Currently Amended) A method as in claim 1, wherein generating includes examining pathways of genes with respect to gene activation sequences; extending said pathway pathways using said gene expression information; and constructing a hypothesized relationship concerning an extension of at least one of said pathways. pathway.

7. (Currently Amended) A method as in claim 1, wherein generating includes evaluating correlation values with respect to an identified gene or gene sequence so as to determine variations in the behavior of said identified gene or gene sequence; and confirming said hypothesized relationship ~~in response to~~ by applying said a statistical technique.

8. (Currently Amended) A method as in claim 1, including wherein the step of identifying includes: rating said hypothesized relationship with a measure of interest by said at least one agent; and ~~determining whether to send said information such that said determination is selecting said at least one agent~~ responsive to said measure.

9. (Currently Amended) A method as in claim 8, including wherein the step of selecting includes: determining a threshold in said measure of interest; and ~~sending said information in a manner responsive to comparing said threshold and said measure of interest.~~

10. (Original) A method as in claim 8, wherein said measure of interest is periodically reevaluated.

11. (Currently Amended) A method as in claim 8, wherein said measure of interest is responsive to whether complexity of said hypothesized relationship, relationship is relatively simple and relatively unlikely to be the likelihood of said hypothesized relationship being due to chance, or whether said hypothesized relationship relates to at least one of: genes one or more researchers have indicated they are interested in, genes for which there are published papers, selected domain-specific knowledge about gene expression.

12. (Canceled).

13. (Currently Amended) A method as in claim 12, 1, wherein said data regarding interests collateral information includes at least one of: information about interests of said at least one agent, information about published papers, information about researchers, information about relationships between genes.

14. (Currently Amended) Apparatus including  
memory recording information about a plurality of gene expression values;  
an autonomous software element disposed on a computing device, said autonomous software element having access to said memory;  
said memory recording information about a hypothesized relationship between said gene expression values, said hypothesized relationship having the properties of being (1) relatively unlikely to be having a likelihood of being due to chance not exceeding a predetermined value, and

(2) satisfying at least one predetermined test indicating that said hypothesized relationship is of potential relatively likely to be of interest to at least one agent other than said autonomous software element; and

a communication link coupled to said memory and capable of sending information about said hypothesized relationship to said at least one agent.

15. (Currently Amended) Apparatus as in claim 14, wherein said communication link is capable of collecting said information about the plurality of gene expression values from a plurality of relatively nonlocal external databases.

16. (Currently Amended) Apparatus as in claim 14, wherein said communication link is capable of collecting said information from at least one external database, relatively nonlocal databases.

17. (Original) Apparatus as in claim 14, wherein  
said hypothesized relationship includes (a) information about a first set of genes, said first set of genes having been selected in response to said gene expression values, and (b) information about a second set of genes, said second set of genes having been selected in response to data other than said gene expression values;

said hypothesized relationship has been confirmed in response to a statistical technique applied to said first set and said second set.

18. (Currently Amended) An apparatus as in claim 14, including  
a means for selecting a first set of genes in response to said gene expression values;  
a means for selecting a second set of genes in response to data other than said gene expression values;  
a means for applying a statistical technique to said first set and said second set; and  
a means for confirming said hypothesized relationship in response to applying said statistical technique.

19. (Original) An apparatus as in claim 14, including  
a means for selecting a set of genes in response to said gene expression values;  
a means for comparing the frequencies of the nucleotide sequences upstream from said set of genes to the frequencies of the nucleotide sequences upstream of genes not in said set; and  
a means for constructing a hypothesis that is responsive to sequences that have an anomalous frequency distribution.

20. (Currently Amended) An apparatus as in claim 14, including  
a means for examining pathways of genes with respect to gene activation sequences;  
a means for extending said pathway pathways using said gene expression information; and  
a means for constructing a hypothesized relationship concerning an extension of at least one of said pathway pathways.

21. (Currently Amended) An apparatus as in claim 14, including

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a means for evaluating correlation values with respect to an identified gene or gene sequence so as to determine variations in the behavior of said identified gene or gene sequence; and  
a means for confirming said hypothesized relationship in response to applying said a statistical technique.

22. (Currently Amended) Apparatus as in claim 14, said memory including information associating said hypothesized relationship with a measure of interest by said agent; and  
a software comparator coupled to said said measure of interest and to a selected threshold.

23. (Original) Apparatus as in claim 14, wherein said autonomous software element has access to collateral information other than gene expression values.

24. (Currently Amended) A memory recording information including instructions, said instructions interpretable by a computing device, said instructions including an autonomous software element having access to information about a plurality of gene expression values;

a first software element coupled to said information and capable of generating a hypothesized relationship between said gene expression values, said hypothesized relationship having the properties of being (1) relatively unlikely to be having a likelihood of being due to chance not exceeding a predetermined value, and (2) satisfying at least one predetermined test indicating that

said hypothesized relationship is of potential relatively likely to be of interest to at least one agent other than said autonomous software element;

a second software element coupled to information about said hypothesized relationship and capable of sending information about said hypothesized relationship to said at least one agent.

25. (Original) A memory as in claim 24, including  
information about a first set of genes selected in response to said gene expression values;  
information about a second set of genes selected in response to data other than said gene expression values;  
information about said hypothesized relationship selected in response to applying a statistical technique to said first set and said second set.

26. (Currently Amended) A memory as in claim 24, wherein generating by the first software element includes  
information about selecting a first set of genes in response to said gene expression values;  
information about selecting a second set of genes in response to data other than said gene expression values;  
information about applying a statistical technique to said first set and said second set; and confirming said hypothesized relationship in response to applying said statistical technique.

27. (Currently Amended) A memory as in claim 24, wherein generating by the first software element includes

~~information about~~ selecting a set of genes in response to said gene expression values;  
~~information about~~ comparing the frequencies of the nucleotide sequences upstream from said set of genes to the frequencies of the nucleotide sequences upstream of genes not in said set; and  
~~information about~~ constructing a hypothesis that is responsive to sequences that have an anomalous frequency distribution.

28. (Currently Amended) A memory as in claim 24, including  
information about examining pathways of genes with respect to gene activation sequences;  
information about extending said pathways pathway using said gene expression information;  
and  
information about constructing a hypothesized relationship concerning an extension of said pathways. pathway.

29. (Currently Amended) A memory as in claim 24, wherein the first software element evaluating evaluates correlation values with respect to an identified gene or gene sequence so as to determine variations in the behavior of said identified gene or gene sequence; and  
confirming confirms said hypothesized relationship in response to applying said a statistical technique.

30. (Currently Amended) A method including

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~~executing, on a computing device, an autonomous software element, said autonomous software element having access to accessing information about concerning a set of genes and proteins;~~

~~generating, in response to said information, generating from said information a hypothesized relationship involving at least one of the following: a set of proteins, SNPs or and chemicals pertaining to said information, said hypothesized relationship having a likelihood of being due to chance not exceeding a predetermined value;~~

~~retrieving data regarding interests of each agent of a plurality of agents;  
identifying at least one agent of the plurality of agents such that the data regarding interests of said at least one agent satisfies at least one predetermined test indicating that said at least one agent has a potential interest in the hypothesized relationship; and~~

~~sending information about said hypothesized relationship to said at least one agent.~~

31. (Currently Amended) A method as in claim 30, including collecting said information from a plurality of ~~relatively nonlocal external~~ databases.

32. (Currently Amended) A method as in claim 30, including collecting said information from at least one ~~relatively nonlocal external~~ database.

33. (Currently Amended) A method as in claim 30, ~~including wherein the step of identifying includes:~~

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rating said hypothesized relationship with a measure of interest by said at least one agent;  
and

~~determining whether to send said information such that said determination is selecting said at least one agent~~ responsive to said measure.

34. (Currently Amended) A method as in 30, ~~including 33, wherein the step of selecting includes:~~

~~determining a threshold in said measure of interest; and sending said information in a manner responsive to comparing said threshold and said measure of interest.~~

35. (Original) A method as in claim 34, wherein said measure of interest is periodically reevaluated.

36. (Canceled).

37. (Currently Amended) A method as in claim 34, wherein said data regarding interests collateral information includes at least one of: information about interests of said at least one agent, information about published papers, information about researchers, information about relationships between genes.